#### Barley Genetics Newsletter (2008) 38:100-102

# Report of the Workshop on Barley Genetic Linkage Groups, Barley Genome, Genes and Genetic Stocks at the X. International Barley Genetics Symposium in Alexandria, Egypt, April 2008.

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#### Agenda:

#### The following topics were brought up for discussion during the workshop:

- 1. The current coordination system of to-day and its function in the future.
- 2. The whole genome coordination.
- 3. Integration of molecular and morphological marker maps.
- 4, Nomination of coordinators.
- 5. Barley Genetics Newsletter.
- 6, The International Database for Barley Genes and Barley Genetic Stocks and GrainGenes.
- 7. Symbolization and nomenclature problems of barley genes.
- 8. Maintenance of barley Genetic Stocks.
- 9. International Overall Coordinator.

#### 1. COORDINATION SYSTEM.

Discussions were focused on its activities of to-day and to-morrow. There are many possible technologies for identifying genes to-day and progress is made in integration of gene based maps especially made by the Scottish Crop Research Institute. Bill Thomas, Scotland, presented past activities how the coordination group was started with initiation on NIL, SNP and AFLP marker integration. When now working on Illumina SNPs marker high throughout genotyping, 15 000 markers, QTLs and other technologies can give us much more information about each chromosome. He also gave an overview of the progress that is done for integration of Gene based maps: (a) 4 500 Illumina SNP markers; (b) 1 000 genes on the IPK Gene Map; (c) 2 500 genes in the Japanese EST map; (d) 1 500 SFP markers; (e) 1 000 Bowman lines mapped with BOPA1 and (f) 11 000 QTLs. It was suggested to have not each chromosome coordinated but store and coordinate all 7 chromosomes together.

#### 2. THE WHOLE GENOME COORDINATION.

Several participants stressed that we also need the whole genome coordination. This should be a team task since the biology of mutants should be evaluated and this is a huge effort and a whole time work. For the time being, the time is not ready for one person to handle this. Therefore the workshop recommended to continue with to-days system. For publications of general QTL locations, the workshop recommended that the estimated Bin map position of the gene/QTL must be included.

#### 3. INTEGRATION OF MOLECULAR AND MORPHOLOGICAL MAPS.

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Andy Kleinhofs, USA, has been trying to integrate molecular and morphological maps for many years with large success. This is of great importance more than ever. There do exist many good maps that could be used as references e.g. SSR maps, DART maps etc. The quality of data of these maps is very high and linkage groups are easily detected. We need all the basic morphological genes with its information and have them in good shape. In the San Diego, USA, meetings, 2008, only very few groups were represented that are working on molecular genotyping. David Marshall, The Scottish Crop Research Institute, Dundee, Scotland, agreed to take over this responsibility.

#### 4. NOMINATION OF COORDINATORS.

In the following, a list of the Chromosome/Linkage Groups and Genetic Stocks Collections is presented with the names of the individuals who agreed to be responsible.

#### a. Overall Chairman and chromosomes:

Overall chairman	Udda Lundqvist, Sweden assisted by: Agnese Kolodinska Brantestam,
	Sweden
Chromosome 1H (5)	Gunter Backes, Denmark
Chromosome 2H	J.D. Franckowiak, Australia
Chromosome 3H	Luke Ramsey, UK.
Chromosome 4H	Arnis Druka, UK. (replaces Brian Forster who resigned)
Chromosome 5H (7)	George Fedak, Canada
Chromosome 6H	Victoria Blake, USA.
Chromosome 7H (1)	Lynn Dahleen. USA.

## **b. Integration of molecular and morphological maps:** David Marshall, UK, (replaces Andy Kleinhofs, USA, who wants to step down).

#### c. Genetic Stocks and Collections:

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Barley Genetic Stock Center:	Harold Bockelman, USA, (replaces An Hang who	
	retired 2007)	
Trisomics and aneuploids:	Harold Bockelman, USA, (replaces An Hang)	
Translocations and BTT:	Andreas Houben, Germany	
Desynaptic Genes:	Andreas Houben, Germany	
Autotetraploids:	Wolfgang Friedt, Germany	
Disease and pest resistance genes:	Mark Sutherland, Australia. (replaces Brian Steffenson,	
	USA, who wants to step down)	
Eceriferum genes:	Udda Lundqvist, Sweden	
Chloroplast genes:	Mats Hanssom, Denmark	
Male sterile genes:	Mario Therrien, Canada	
Spike morphology genes:	Udda Lundqvist, Sweden and Michele Stanca, Italy	
Semi-dwarf genes:	J. D. Franckowiak, Australia	
Early maturity genes:	Udda Lundqvist, Sweden	
Barley-wheat genetic stocks:	A.K.M.R. Islam, Australia	

Coordinators are expected to conduct current literature searches and such research in their area of responsibility. Updated information should be published in Barley Genetics Newsletter annually.

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#### 5. BARLEY GENETICS NEWSLETTER.

Barley Genetics Newsletter (BGN) has been established in 1970 after decisions made at the 2nd International Barley Genetics Symposium (IBGS) in Pullman, USA, with its first volume 1971. The original idea was to report short preliminary barley research notes, descriptions of barley genes and stocks, chromosome locations, barley maps and literature references. One of the initiators, Bob Nilan, USA, of the Newsletter and the IBGS was attending the workshop and became acknowledged. After some discussions and opinions the workshop decided strongly to continue the BGN in electronic format as it is the only forum for the barley community publishing updated revised gene descriptions and short notes. Phil Bregitzer, USA, is continuing to act as main editor. Its availability should be more announced and reminders for submissions will be send several times a year.

### 6. INTERNATIONAL DATABASE FOR BARLEY GENES AND BARLEY GENETIC STOCKS AND GRAINGENES.

Udda Lundqvist gave a short demonstration of this database with its own special address <a href="www.untamo.net.bgs">www.untamo.net.bgs</a>. Most parts are linked to GrainGenes. Several participants in the workshop stressed that both databases are not easy and simple to use and rather time consuming. If you are familiar with barley nomenclature, genetics and Bin maps you get the information you need. Victoria Blake, USA, the coordinator for GrainGenes, promised when getting suggestions, to improve the use.

#### 7. SYMBOLIZATION AND NOMENCLATURE PROBLEMS OF BARLEY GENES.

Udda Lundqvist informed of germplasm problems in connection with the Untamo database that Morten Huldén (the former head of the information department at the Nordic Genetic Resource Center and now responsible for this database) ran into when he was including revised descriptions.

- (a). Germplasm stocks should get assigned a GSHO number and seed samples should have been submitted to the Stock Center before descriptions are published.
- (b). References as 'unpublished' and 'personal communication' should be avoided.
- (c). No clear definitions of disease and pest resistance genes.
- (d). When revising a gene and moved from one locus to another, both descriptions should be revised and published.

In the discussions several participants agreed that in many cases the rules for assigning genes, alleles and germplasm stock numbers have not been taken notice on. Especially the nomenclature rules for pest and resistance genes failed to follow, the former coordinator stressed that this nomenclature exists for a long time, nobody wants to do the allelic tests, people usually have not checked the literature and just assigned temporary names in order not to miss the allele. The new coordinator urgently asked that new resistant names, genes and symbols should first be accepted by the coordinator before publishing.

The workshop also recommended strongly to publish the rules annually in Barley Genetics Newsletter.

#### 8. MAINTENANCE OF BARLEY GENETIC STOCKS.

The workshop acknowledged the existence of different barley collections world-wide, its necessity to maintain and keep them in good shape and update all information continuously.

#### 9. INTERNATIONAL OVERALL COORDINATOR.

The workshop recommended that the to-days chairman for the barley linkage groups and collections should continue.